

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/419,305

DATE: 02/15/2000
TIME: 19:00:20

INPUT SET: S34768.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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(1) General Information:

(i) APPLICANT: MARUTA, Kazuhiko
KUBOTA, Michio
SUGIMOTO, Toshiyuki

ENTERED

(ii) TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
FORMS NON-REDUCING SACCHARIDE FROM REDUCING AMYLACEOUS
SACCHARIDE

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Browdy and Neimark
(B) STREET: 419 Seventh Street N.W. Ste. 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/419,305
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/505,448
(B) FILING DATE: 21-JUL-1994
(A) APPLICATION NUMBER: JP 190183/1994
(B) FILING DATE: 21-JUL-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 189706/1995
(B) FILING DATE: 04-JUL-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Browdy, Roger L.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/419,305DATE: 02/15/2000
TIME: 19:00:21

INPUT SET: S34768.raw

47 (B) REGISTRATION NUMBER: 25,618
48 (C) REFERENCE/DOCKET NUMBER: MARUTA=3
49
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: (202) 628-5197
52 (B) TELEFAX: (202) 737-3528
53
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55
56 (2) INFORMATION FOR SEQ ID NO:1:
57
58 (i) SEQUENCE CHARACTERISTICS:
59 (A) LENGTH: 720 amino acids
60 (B) TYPE: amino acid
61 (D) TOPOLOGY: linear
62
63 (ii) MOLECULE TYPE: protein
64
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67 Val Ile Ser Ala Thr Tyr Arg Leu Gln Leu Asn Lys Asn Phe Asn Phe
68 1 5 10 15
69
70 Gly Asp Val Ile Asp Asn Leu Trp Tyr Phe Lys Asp Leu Gly Val Ser
71 20 25 30
72
73 His Leu Tyr Leu Ser Pro Val Leu Met Ala Ser Pro Gly Ser Asn His
74 35 40 45
75
76 Gly Tyr Asp Val Ile Asp His Ser Arg Ile Asn Asp Glu Leu Gly Gly
77 50 55 60
78
79 Glu Lys Glu Tyr Arg Arg Leu Ile Glu Thr Ala His Thr Ile Gly Leu
80 65 70 75 80
81
82 Gly Ile Ile Gln Asp Ile Val Pro Asn His Met Ala Val Asn Ser Leu
83 85 90 95
84
85 Asn Trp Arg Leu Met Asp Val Leu Lys Met Gly Lys Lys Ser Lys Tyr
86 100 105 110
87
88 Tyr Thr Tyr Phe Asp Phe Phe Pro Glu Asp Asp Lys Ile Arg Leu Pro
89 115 120 125
90
91 Ile Leu Gly Glu Asp Leu Asp Thr Val Ile Ser Lys Gly Leu Leu Lys
92 130 135 140
93
94 Ile Val Lys Asp Gly Asp Glu Tyr Phe Leu Glu Tyr Phe Lys Trp Lys
95 145 150 155 160
96
97 Leu Pro Leu Thr Glu Val Gly Asn Asp Ile Tyr Asp Thr Leu Gln Lys
98 165 170 175
99

RAW SEQUENCE LISTING PATENT APPLICATION US/09/419,305

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 TIME: 19:00:21

INPUT SET: S34768.raw

100	Gln	Asn	Tyr	Thr	Leu	Met	Ser	Trp	Lys	Asn	Pro	Pro	Ser	Tyr	Arg	Arg
101				180					185					190		
102																
103	Phe	Phe	Asp	Val	Asn	Thr	Leu	Ile	Gly	Val	Asn	Val	Glu	Lys	Asp	His
104			195					200					205			
105																
106	Val	Phe	Gln	Glu	Ser	His	Ser	Lys	Ile	Leu	Asp	Leu	Asp	Val	Asp	Gly
107		210					215					220				
108																
109	Tyr	Arg	Ile	Asp	His	Ile	Asp	Gly	Leu	Tyr	Asp	Pro	Glu	Lys	Tyr	Ile
110	225					230					235					240
111																
112	Asn	Asp	Leu	Arg	Ser	Ile	Ile	Lys	Asn	Lys	Ile	Ile	Ile	Val	Glu	Lys
113					245					250					255	
114																
115	Ile	Leu	Gly	Phe	Gln	Glu	Glu	Leu	Lys	Leu	Asn	Ser	Asp	Gly	Thr	Thr
116				260					265					270		
117																
118	Gly	Tyr	Asp	Phe	Leu	Asn	Tyr	Ser	Asn	Leu	Leu	Phe	Asn	Phe	Asn	Gln
119			275					280					285			
120																
121	Glu	Ile	Met	Asp	Ser	Ile	Tyr	Glu	Asn	Phe	Thr	Ala	Glu	Lys	Ile	Ser
122		290					295					300				
123																
124	Ile	Ser	Glu	Ser	Ile	Lys	Lys	Ile	Lys	Ala	Gln	Ile	Ile	Asp	Glu	Leu
125	305					310					315					320
126																
127	Phe	Ser	Tyr	Glu	Val	Lys	Arg	Leu	Ala	Ser	Gln	Leu	Gly	Ile	Ser	Tyr
128					325					330					335	
129																
130	Asp	Ile	Leu	Arg	Asp	Tyr	Leu	Ser	Cys	Ile	Asp	Val	Tyr	Arg	Thr	Tyr
131				340					345					350		
132																
133	Ala	Asn	Gln	Ile	Val	Lys	Glu	Cys	Asp	Lys	Thr	Asn	Glu	Ile	Glu	Glu
134			355					360					365			
135																
136																
137	Ala	Thr	Lys	Arg	Asn	Pro	Glu	Ala	Tyr	Thr	Lys	Leu	Gln	Gln	Tyr	Met
138		370					375					380				
139																
140	Pro	Ala	Val	Tyr	Ala	Lys	Ala	Tyr	Glu	Asp	Thr	Phe	Leu	Phe	Arg	Tyr
141	385					390				395						400
142																
143	Asn	Arg	Leu	Ile	Ser	Ile	Asn	Glu	Val	Gly	Ser	Asp	Leu	Arg	Tyr	Tyr
144					405					410					415	
145																
146	Lys	Ile	Ser	Pro	Asp	Gln	Phe	His	Val	Phe	Asn	Gln	Lys	Arg	Arg	Gly
147				420					425					430		
148																
149	Lys	Ile	Thr	Leu	Asn	Ala	Thr	Ser	Thr	His	Asp	Thr	Lys	Phe	Ser	Glu
150			435					440					445			
151																
152	Asp	Val	Arg	Met	Lys	Ile	Ser	Val	Leu	Ser	Glu	Phe	Pro	Glu	Glu	Trp

RAW SEQUENCE LISTING PATENT APPLICATION US/09/419,305

DATE: 02/15/2000
TIME: 19:00:21

INPUT SET: S34768.raw

153	450	455	460
154			
155	Lys Asn Lys Val Glu Glu Trp His Ser Ile Ile Asn Pro Lys Val Ser		
156	465	470	475 480
157			
158	Arg Asn Asp Glu Tyr Arg Tyr Tyr Gln Val Leu Val Gly Ser Phe Tyr		
159		485 490	495
160			
161	Glu Gly Phe Ser Asn Asp Phe Lys Glu Arg Ile Lys Gln His Met Ile		
162		500 505	510
163			
164	Lys Ser Val Arg Glu Ala Lys Ile Asn Thr Ser Trp Arg Asn Gln Asn		
165		515 520	525
166			
167	Lys Glu Tyr Glu Asn Arg Val Met Glu Leu Val Glu Glu Thr Phe Thr		
168		530 535	540
169			
170	Asn Lys Asp Phe Ile Lys Ser Phe Met Lys Phe Glu Ser Lys Ile Arg		
171		545 550	555 560
172			
173	Arg Ile Gly Met Ile Lys Ser Leu Ser Leu Val Ala Leu Lys Ile Met		
174		565 570	575
175			
176	Ser Ala Gly Ile Pro Asp Phe Tyr Gln Gly Thr Glu Ile Trp Arg Tyr		
177		580 585	590
178			
179	Leu Leu Thr Asp Pro Asp Asn Arg Val Pro Val Asp Phe Lys Lys Leu		
180		595 600	605
181			
182	His Glu Ile Leu Glu Lys Ser Lys Lys Phe Glu Lys Asn Met Leu Glu		
183		610 615	620
184			
185	Ser Met Asp Asp Gly Arg Ile Lys Met Tyr Leu Thr Tyr Lys Leu Leu		
186		625 630	635 640
187			
188	Ser Leu Arg Lys Gln Leu Ala Glu Asp Phe Leu Lys Gly Glu Tyr Lys		
189		645 650	655
190			
191	Gly Leu Asp Leu Glu Glu Gly Leu Cys Gly Phe Ile Arg Phe Asn Lys		
192		660 665	670
193			
194	Ile Leu Val Ile Ile Lys Thr Lys Gly Ser Val Asn Tyr Lys Leu Lys		
195		675 680	685
196			
197	Leu Glu Glu Gly Ala Ile Tyr Thr Asp Val Leu Thr Gly Glu Glu Ile		
198		690 695	700
199			
200	Lys Lys Glu Val Gln Ile Asn Glu Leu Pro Arg Ile Leu Val Arg Met		
201		705 710	715 720
202			
203			
204	(2) INFORMATION FOR SEQ ID NO:2:		
205			

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/419,305DATE: 02/15/2000
TIME: 19:00:22

INPUT SET: S34768.raw

206 (i) SEQUENCE CHARACTERISTICS:
207 (A) LENGTH: 2160 base pairs
208 (B) TYPE: nucleic acid
209 (C) STRANDEDNESS: single
210 (D) TOPOLOGY: linear
211
212 (ii) MOLECULE TYPE: cDNA
213
214
215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
216
217 GTGATATCAG CAACCTACAG ATTACAGTTA AATAAGAATT TTAATTTTGG TGACGTAATC 60
218
219 GATAACCTAT GGTATTTTAA GGATTTAGGA GTTTCCTATC TCTACCTCTC TCCTGTCTTA 120
220
221 ATGGCTTCGC CAGGAAGTAA CCATGGGTAC GATGTAATAG ATCATTCAAG GATAAACGAT 180
222
223 GAACTTGGAG GAGAGAAAGA ATACAGGAGA TTAATAGAGA CAGCTCATACT TATTGGATTA 240
224
225 GGTATTATAC AGGACATAGT ACCAAATCAC ATGGCTGTAA ATTCTCTAAA TTGGCGACTA 300
226
227 ATGGATGTAT TAAAAATGGG TAAAAAGAGT AAATATTATA CGTACTTTGA CTTTTTCCCA 360
228
229 GAAGATGATA AGATACGATT ACCCATATTA GGAGAAGATT TAGATACAGT GATAAGTAAA 420
230
231 GGTTTATTAA AGATAGTAAA AGATGGAGAT GAATATTTCC TAGAATATTT CAAATGGAAA 480
232
233 CTCCTCTAA CAGAGGTTGG AAATGATATA TACGACACTT TACAAAAACA GAATTATACC 540
234
235 CTAATGTCTT GGAAAAATCC TCCTAGCTAT AGACGATTCT TCGATGTTAA TACTTTAATA 600
236
237 GGAGTAAATG TCGAAAAAGA TCACGTATTT CAAGAGTCCC ATTCAAAGAT CTTAGATTTA 660
238
239 GATGTTGATG GCTATAGAAT TGATCATATT GATGGATTAT ATGATCCTGA GAAATATATT 720
240
241 AATGACCTGA GGTCAATAAT TAAAAATAAA ATAATTATTG TAGAAAAAAT TCTGGGATTT 780
242
243 CAGGAGGAAT TAAAATTAAA TTCAGATGGA ACTACAGGAT ATGACTTCTT AAATTACTCC 840
244
245 AACTTACTGT TTAATTTTAA TCAAGAGATA ATGGACAGTA TATATGAGAA TTTCACAGCG 900
246
247 GAGAAAAATAT CTATAAGTGA AAGTATAAAG AAAATAAAAG CGCAAATAAT TGATGAGCTA 960
248
249 TTTAGTTATG AAGTTAAAAG ATTAGCATCA CAACTAGGAA TTAGCTACGA TATATTGAGA 1020
250
251 GATTACCTTT CTTGTATAGA TGTGTACAGA ACTTATGCTA ATCAGATTGT AAAAGAGTGT 1080
252
253 GATAAGACCA ATGAGATAGA GGAAGCAACC AAAAGAAATC CAGAGGCTTA TACTAAATTA 1140
254
255 CAACAATATA TGCCAGCAGT ATACGCTAAA GCTTATGAAG ATACTTTCCT CTTTAGATAC 1200
256
257 AATAGATTAA TATCCATAAA TGAGGTTGGA AGCGATTTAC GATATTATAA GATATCGCCT 1260
258

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/419,305

DATE: 02/15/2000
TIME: 19:00:22

INPUT SET: S34768.raw

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